

SC galactose, 100 mM KCl

SC glucose, 0mM KCl

SC galactose, 0 mM KCl

SC glucose, 100 mM KCl

FIG. 1

08816011-031197



330 Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg  
TAC ACA CTG CCA CGT TCC AAT TCG TGT CCG GAT CTG AGC ATG TAC TAC CCG GTG GAG CCG GCT CCC ATT CCC AGC CGG 1050

360 Lys Arg Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly Met Val His Ala Asn Ser Asp  
AAG AGG GCA TTC TCC GTG TGC GCC GAC ATG GTT GGC CCA AGG GAG GCG GTG GTA CAC GCC AAT TCC GAT 1125

380 Thr Asp Leu Thr Lys Leu Asp Arg Glu Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu  
ACG GAT CTA ACC AAA CTG GAT CGC GAG AAG ACA TTC GAG ACG GCG GCG TAC CAC CAG CAG ACC ACC GAT TTG CTG 1200

410 Ala Lys Val Asn Ala Leu Ala Thr Val Lys Pro Pro Ala Glu Gln Glu Asp Ala Ala Leu Cys Tyr Gly Gly  
GCC AAG GTG GTC AAC GCA CTG GCC ACC GTG AAG CCA CCG CCG GCG GAA GAT GCG GCT CTT TAT GGT GGC 1275

430 Tyr His Gly Phe Ser Asp Ser Gln Ile Leu Ala Ser Ser Asp Phe Asn Leu Glu Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg  
TAT CAT GAC TTC TCC GAC TCC CAG ATC CTG GCC AGC GAA TGG TCG TTC TCG ACG GTC AAC GAG TTC ACA TCA CCG 1350

460 Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg  
CGA CGT CCA AGA GCA GCA CGT GCC TCC GAT TTC AAT CTG GAG GCA CCT CCG TGG CAG AGC GAG CCA CTG CGT 1425

480 Ser Ser His Asn Glu Trp Thr Trp Ser Gly Asp Asn Gln Gln Ile Gln Glu Ala Phe Asn Gln Arg Tyr Lys Gly  
TCG AGC CAC AAC GAA TGG ACA TGG AGC GGC GAC AAC CAG CAG ATC CAG GAG GCA TTC AAC CAG CCG TAC AAG GGA 1500

510 Gln Gln Arg Ala Asn Gly Ala Ala Asn Ser Thr Met Val His Leu Glu Pro Asp Ala Leu Glu Gln Leu Arg  
CAG CAG CGT GCC AAC GGA GCA GCC AAC TCG ATG ATC TCT CAT CTG GAG CCG GAT GCT TTG GAG GAG CAG CTG AGA 1575

530 Asn Asn His Arg Val Pro Val Ala Ser Arg Ser Ser Pro Cys Arg Met Val Cys Asp Val Cys Phe Pro Ser Arg  
AAC AAT CAC CCG GTG CCG GTC CCG TCA AGA AGT TCT CCA TCG CCG ATG GTC TCG GAC GTC TGT TTC CCT TCC AGA 1650

560 Arg Ser Thr Pro Arg Arg Ile Trp Ser Ala Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys  
AGA AGC ACC CCT CGC AGG ATC TGG AGC GCA AGT TGT CCG TGG TCT CCG TAC CCG AGG GTG TCA TCT CGC AGG AAG 1725

580 Pro Asp Pro Arg Trp Thr Thr Thr Ser Thr Arg Ser Arg Arg Pro Pro Val Asn Pro Ile Cys Ala Thr Asp Ala  
CCA GAT CCC CGC TGG ACT ACA TCA ACA CCG TCA CCG CGC CCT CCA GTC AAT CCT AIT TGC GCA ACG GAC GCG 1800

610 Val Arg His Arg Pro Ser Asn Arg Met Ala Ala Trp Pro Ala Ala Cys Ala Gly  
GTC CGC CAC CGC CCT TCG AAT CGA ATG GCA GCT TGG CCA GCG GCG GCG TAA CGAACAATGGGCTTCAGATGGAG 1880

GATGAGCACCCTCCGATTCGGCGTGCAGCCTATCAACGCAAGCGGCTGTGCGAGCGCGGAGAGCATCTACACCCAGCAATCAA  
GCCCCATCGCTGCGCGGAGCAGATGTTCCCGCCAGCGCAGCGCTTCGCGCCAGATGAGCGGCGGCTTGGCACCAGCTGGCTTGGGA  
TCGGCGCATTCGCGCGCGCTGTGGAGCCTTTCGCCAGCTACAGATGGGATCATCGCTGACCTGTCTCGCGCGGAGCAGCATTA  
TTCTCGGTACCTCCGAAAGGATATGAATGTGCTGGAGCAGACGACCATTCGAGTATGATTGTGCGCTGGAG . . . 3.

FIG. 2B

10  
 Met Ser Asp Gln Leu Phe Val Ala Phe Glu Lys Tyr Phe Leu Thr Ser Asn Glu Val Lys  
 20  
 ATG TCC GAT CAG CTG TTT GTC GCA TTT GAG AAG TAT TTC TTG ACG AGT AAC GAG GTC AAG  
 30  
 Lys Asn Ala Ala thr Glu Thr Trp Thr Phe Ser Ser Ser Ile Phe Phe Ala Val Thr Val  
 40  
 AAG AAT GCA GCA ACG GAG ACA TGG ACA TTT TCA TCG TCC ATT TTC TTT GCC GTA ACC GTC  
 50  
 H5-1  
 Val Thr Thr Ile Glv Tyr Glv Asn Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys  
 60  
 GTC ACT ACC ATC GGA TAC GGT AAT CCA GTT CCA CTG ACA AAC ATT GCA CCG ATA TGG TGT  
 70  
 M2  
 Ile Leu Phe Ser Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Asp Leu Ala Gly  
 80  
 ATA TTG TTC TCC TTG CTT GGA ATA CCT CTA ACA CTG GTT ACC ATC GCT GAC TTG GCA GGT  
 90  
 Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys Leu Lys Tyr Leu  
 100  
 AAA TTC CTA TCT GAA CAT CTT GTT TGG TTG TAT GGA AAC TAT TTG AAA TTA AAA TAT CTC  
 110  
 Ile Leu Ser Arg His Arg Lys Glu Arg Glu His Val Cys Glu His Cys His Ser His  
 120  
 ATA TTG TCA CGA CAT CGA AAA GAA CGG AGA GAG CAC GTT TGT GAG CAC TGT CAC AGT CAT  
 130  
 Gly Met Gly His Asp Met Asn Ile Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala  
 140  
 GGA ATG GGG CAT GAT ATG AAT ATC GAG GAG AAA AGA ATT CCT GCA TTC CTG GTA TTA GCT  
 150  
 M3  
 Ile Leu Ile Val Tyr Thr Ala Phe Glv Val Leu Met Ser Lys Leu Glu Pro Trp Ser  
 160  
 ATT CTG ATA GTA TAT ACA GCG TTT GCG GGT GTC CTA ATG TCA AAA TTA GAG CCG TGG TCT  
 180  
 240  
 300  
 360  
 420  
 480

FIG. 3A

170	H5-2	180
Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Glv Phe Glv Asp Leu		
TTC TTC ACT TCA TTC TAC TGG TCC TTC ATT ACA ATG ACT ACT CTC GGG TTT GGC GAC TTG		540
190		200
Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu Leu Tyr Ile Ile Leu Gly Lys Phe		
ATG CCC AGA AGG GAC GGA TAC ATG TAT ATC ATA TTG CTC TAT ATC ATT TTA GGT AAA TTT		600
210		220
Ser Met Lys Lys Lys Gln Lys Phe Lys Ile Phe Leu Glv Leu Ala Ile Thr Thr Met Cys		
TCA ATG AAA AAA AAA CAA AAA TTC AAA ATA TTT TTA GGT CTT GCA ATA ACT ACA ATG TGC		660
230		240
Ile Asp Leu Val Glv Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln		
ATT GAT TTG GTA GGA GTA CAG TAT ATT CGA AAG ATT CAT TAT TTC GGA AGA AAA ATT CAA		720
250		260
Asp Ala Arg Ser Ala Leu Ala Val Val Gly Lys Val Val Leu Val Ser Glu Leu Tyr		
GAC GCT AGA TCT GCA TTG GCG GTT GTA GGA GGA AAG GTA GTC CTT GTA TCA GAA CTC TAC		780
270		280
Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser Arg Glu Ala Phe Ile Val Glu Asn		
GCA AAT TTA ATG CAA AAG CGA GCT CGT AAC ATG TCC CGA GAA GCT TTT ATA GTG GAG AAT		840
290		300
Leu Tyr Val Ser Lys His Ile Ile Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr		
CTC TAT GTT TCC AAA CAC ATC ATA CCA TTC ATA CCA ACT GAT ATC CGA TGT ATT CGA TAT		900
310		320
Ile Asp Gln Thr Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ala Ile Asp Met Gln		
ATT GAT CAA ACT GCC GAT GCT ACC ATT TCC ACG TCA TCG TCT GCA ATT GAT ATG CAA		960
330		336
Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys		
AGT TGT AGA TTT TGT CAT TCA AGA TAT TCT CTC AAT CGT GCA TTC AAA TAG		1011

FIG. 3B

Ce orf1 -----  
 Dm orf1 MSPNRRWILL IFYISYLMFG AAIYYHIEHG EEKISRAEQR KAQIAINEYL 50  
 Consensus ..... 50

Ce orf1 ----- --MSDQLFVA FEKYFLTSNE VKKNAATE TW TFSSS FFAV 38  
 Dm orf1 LEELGDKNTT TQDEILQRIS DYCDKPVTLPT PYDDTPYTW TFYHAF FFAF 100  
 Consensus ..... TW TF ... FFA 100

Ce orf1 TWVTITGYGN PVEMTNIGRI WCILFSLIGI PLTLVTIACL AGKFLSEHLV 88  
 Dm orf1 TVCSTVGYGN ISEHITFAGRM IMIAYSVIGI PVNGILFACL ----- 140  
 Consensus TV . T . GYGN . E . T . GR . . . U . S . GI P . . . A . L . 150

Ce orf1 WLYGNVLLKLK YLILSRHKE RREHVCEHCH SHGMCHDMNI EEKHIPAFV 138  
 Dm orf1 ---GSEYFGRT FEAIYRRAKK YKMSTDMHYV PPQLQLITTV VIALIPGIAL 187  
 Consensus . . G . Y . . . . . R . K . . . . . H . . . . . S . . . . . IP . . . 200

Ce orf1 LAIDLIVYTAF GGVLMKLEP WSFFTSFYAS FIVMTTGFG CLMPRLQYM 188  
 Dm orf1 FLVLPVGVH LLRELGLSS- ---ISLYMS YVITTTTCFG DYVET-FOAN 231  
 Consensus . . . L . . . . . S . Y . S . . T . TT . GFG D . B . . G . . 250

Ce orf1 YIILLYILG KFSMKKKQKF KIFLGLAITT MCIDLVMQY IRKIHYFGRK 238  
 Dm orf1 QPKEFGGVFV VYQIFVIWF IFSLGYLVMI MTFITRGLCS KKLAYLEQQL 281  
 Consensus . . . . . F . . . LG . . . M . . . G . Q . . 300

Ce orf1 IQDARSALAV VGGKVLVSE LYANLMQKRA RNMSREAFIV ENLYVSKHII 288  
 Dm orf1 SSNLKATQNR IWSGVTKDVG YLRRLNELY ILKVKPVYTD VDIAYTLPRS 331  
 Consensus . . . . . V . . . . . 350

Ce orf1 PFIFPTDIRCI -RYIDQTADA ATISTSSSAI DMGSCRFCHS RYSLNRAFKK 337  
 Dm orf1 NSCFPLSMYR VEPAPIPSRK RAESVCADMV GAGREAGMVH ANSDTDLTKL 381  
 Consensus . . . R . . . . . S . . . . . C . . . . . S . . . . . K . 400

Ce orf1 ----- 337  
 Dm orf1 DREKTFETAE AYHQTDDL A KVVNALATVK PPPAEQEDAA LYGGYHGFS D 431  
 Consensus ..... 450

Ce orf1 ----- 337  
 Dm orf1 SQILASEWSF STVNEFTSPR RPRARACSDF NLEAPRWQSE RPLRSSHNEW 481  
 Consensus ..... 500

FIG. 4

mIRK  
hROMK1  
rGIRK1

Dm H5-1

Shak  
Shal  
Shab  
Shaw  
Eag  
Slo

Dm H5-2

Dm H5-1  
Ce 5-1  
Dm H5-2  
Ce H5-2

AFLFSIETQTTIGYGFRVCVTDECP  
AFLFSLETQVTIGYGFRVCVEQCA  
AFLFFIETEATIGYGYRYITDHCP

|||||  
AFFFFAFTVCSTVGYGNISPTTFAG  
|||||  
AFWWAVVTMTTVGYGDMTPVGFWG  
AFWYTIVTMTTLGYGDMVPETIAG  
AFWWAGITMTTVGYGDICPTTALG  
GLWWALVTMTTVGYGDMAPKTYIG  
ALYFTMTCMTSVGFGNVAAETDNE  
CVYFLIVTMSTVGYGDVYCETVLG  
|||||  
SLYTSYVTTTTIGFGDYVPTFGAN

{G,A,S,T}, {D,E}  
{N,Q}, {K,R,H}  
{F,Y,W}={I,L,M,V}

AFFFAFTVCSTVGYGNISPTTFAG  
SIFFAVTVTTTIGYGNPVPVTNTG  
SLYTSYVTTTTIGFGDYVPTFGAN  
SFYWSFI TMTTVGFGDLMPPRDGY

FIG. 5A

261120\*11091880

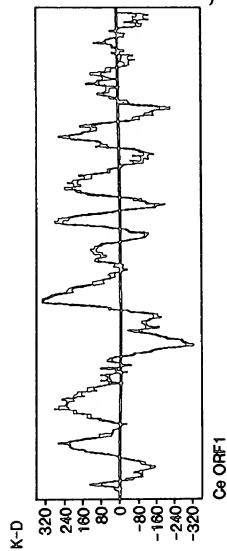
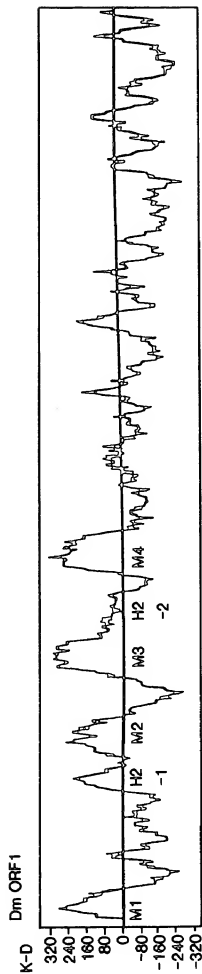
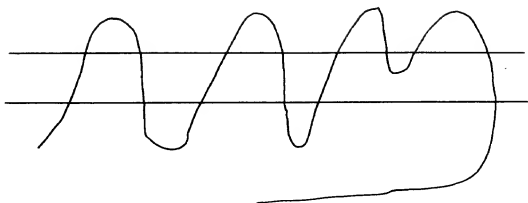


FIG. 5B

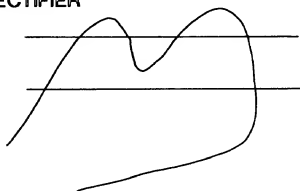


08816011.031197

1) SHAKER



2) INWARD RECTIFIER



3) ORF1

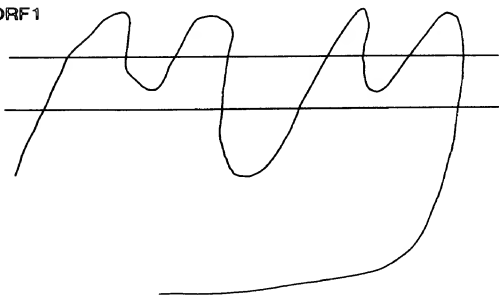


FIG. 6

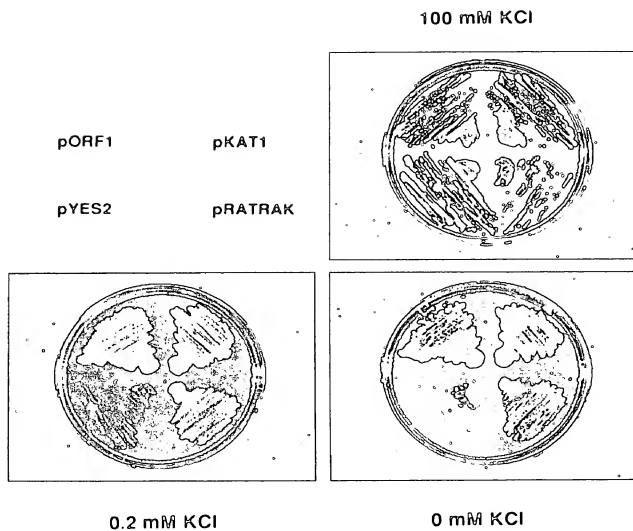
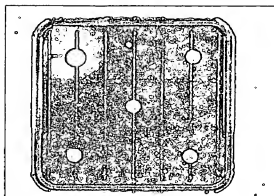


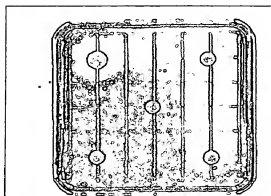
FIG. 7

08816011.031197

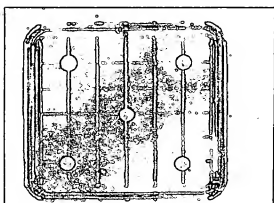
pORF1



pKAT1



pRATRAK



pYES2

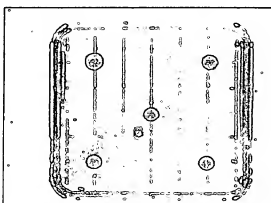


FIG. 8



230 Tyr His Tyr His His Gln Lys Gly Met Glu Ile Arg Glu Lys Ala Glu Thr Asp Arg Pro Ser Pro Ser Ile Leu  
 TAC CAC TAT CAC CAT CAA AAA GGA ATG GAA ATT CGC GAA AAG GCG GAA ACC GAC AGA CCG TCT CCA TCC ATT CTT 750  
  
 240 Trp Thr Thr Phe Thr Asn Cys Tyr Gly Gln Leu Phe Asn Val Trp Phe Cys Phe Ala Val Thr Leu Thr Ile Phe  
 TGG ACC ACA TTC ACA AAC TGT TAT GGG CAA CTC TTC AAT GTT TGG TTC TGC TTT GCC GTT ACT CTC ACA ATC TTC 825  
  
 260 Pro Val Met Met Thr Val Thr Thr Arg Gly Asp Ser Gly Phe Leu Asn Lys Ile Met Ser Glu Asn Asp Glu Ile  
 CCT GTT ATG ATG ACC GTT ACC ACT CGT GGA GAT TCC GGC TTC CTA AAC AAA ATT ATG TCT GAA AAC GAT GAA ATC 900  
  
 280 Tyr Thr Leu Leu Thr Ser Phe Leu Val Phe Asn Leu Phe Ala Ala Ile Gly Ser Ile Val Ala Ser Lys Ile His  
 TAC ACT TTG CTC ACA AGT TTC CTC GTC TTC AAT TTG TTC GCT GCG ATT GGA TCC ATA GTT GCT TCC AAG ATT CAC 975  
  
 300 Trp Pro Thr Pro Arg Tyr Leu Lys Phe Ala Ile Ile Leu Arg Ala Leu Phe Ile Pro Phe Phe Phe Cys Asn  
 TGG CCG ACA CCC CGT TAC CTC AAA TTT GCC ATA ATC TTG CGT GCT CTT TTC ATT CCA TTC TTC TTC TGC AAC 1050  
  
 320 Tyr Arg Val Gln Thr Arg Ala Tyr Pro Val Phe Phe Glu Ser Thr Asp Ile Phe Val Ile Gly Gly Ile Ala Met  
 TAT CGT GTC CAG ACG CGT GCT TAT CCT GTT TTC TTT GAG TCT ACT GAC ATT TTT GTG ATT GGT GGA ATT GCC ATG 1125  
  
 340 Ser Phe Ser His Gly Tyr Leu Ser Ala Leu Ala Met Gly Tyr Thr Pro Asn Val Val Pro Ser His Tyr Ser Arg  
 TCT TTT TCA CAT GGA TAC CTC ACG GCT GCT GCA ATG GGA TAC ACT CCA AAC GTC GTG CCA TCT CAC TAC TCA AGA 1200  
  
 360 Phe Ala Ala Gln Leu Ser Val Cys Thr Leu Met Val Gly Leu Leu Thr Gly Gly Leu Trp Pro Val Val Ile Glu  
 TTT GCC GCT CAG CTT TCC GTT TGC ACT CTT ATG GTT GGC CTT CTC ACC GGT GGC CTG TGG CCC GTT GTT ATT GAG 1275  
  
 380 His Phe Val Asp Lys Pro Ser Ile Leu  
 CAC TTC GTG GAC AAG CCA AGT ATC TTA ATA ATATTATAGCATTAGAGTACTCTGTATATCTGTTTATTTTATTAAGCTGGGATAAA 1364  
  
 400  
 420  
 440  
 460  
 480  
 500  
 520  
 540  
 560  
 580  
 600  
 620  
 640  
 660  
 680  
 700  
 720  
 740  
 760  
 780  
 800  
 820  
 840  
 860  
 880  
 900  
 920  
 940  
 960  
 980  
 1000  
 1020  
 1040  
 1060  
 1080  
 1100  
 1120  
 1140  
 1160  
 1180  
 1200  
 1220  
 1240  
 1260  
 1280  
 1300  
 1320  
 1340  
 1360  
 1380  
 1400  
 1420  
 1440  
 1460  
 1480  
 1500  
 1520  
 1540  
 1560  
 1580  
 1600  
 1620  
 1640  
 1660  
 1680  
 1700  
 1720  
 1740  
 1760  
 1780  
 1800  
 1820  
 1840  
 1860  
 1880  
 1900  
 1920  
 1940  
 1960  
 1980  
 2000  
 2020  
 2040  
 2060  
 2080  
 2100  
 2120  
 2140  
 2160  
 2180  
 2200  
 2220  
 2240  
 2260  
 2280  
 2300  
 2320  
 2340  
 2360  
 2380  
 2400  
 2420  
 2440  
 2460  
 2480  
 2500  
 2520  
 2540  
 2560  
 2580  
 2600  
 2620  
 2640  
 2660  
 2680  
 2700  
 2720  
 2740  
 2760  
 2780  
 2800  
 2820  
 2840  
 2860  
 2880  
 2900  
 2920  
 2940  
 2960  
 2980  
 3000  
 3020  
 3040  
 3060  
 3080  
 3100  
 3120  
 3140  
 3160  
 3180  
 3200  
 3220  
 3240  
 3260  
 3280  
 3300  
 3320  
 3340  
 3360  
 3380  
 3400  
 3420  
 3440  
 3460  
 3480  
 3500  
 3520  
 3540  
 3560  
 3580  
 3600  
 3620  
 3640  
 3660  
 3680  
 3700  
 3720  
 3740  
 3760  
 3780  
 3800  
 3820  
 3840  
 3860  
 3880  
 3900  
 3920  
 3940  
 3960  
 3980  
 4000  
 4020  
 4040  
 4060  
 4080  
 4100  
 4120  
 4140  
 4160  
 4180  
 4200  
 4220  
 4240  
 4260  
 4280  
 4300  
 4320  
 4340  
 4360  
 4380  
 4400  
 4420  
 4440  
 4460  
 4480  
 4500  
 4520  
 4540  
 4560  
 4580  
 4600  
 4620  
 4640  
 4660  
 4680  
 4700  
 4720  
 4740  
 4760  
 4780  
 4800  
 4820  
 4840  
 4860  
 4880  
 4900  
 4920  
 4940  
 4960  
 4980  
 5000  
 5020  
 5040  
 5060  
 5080  
 5100  
 5120  
 5140  
 5160  
 5180  
 5200  
 5220  
 5240  
 5260  
 5280  
 5300  
 5320  
 5340  
 5360  
 5380  
 5400  
 5420  
 5440  
 5460  
 5480  
 5500  
 5520  
 5540  
 5560  
 5580  
 5600  
 5620  
 5640  
 5660  
 5680  
 5700  
 5720  
 5740  
 5760  
 5780  
 5800  
 5820  
 5840  
 5860  
 5880  
 5900  
 5920  
 5940  
 5960  
 5980  
 6000  
 6020  
 6040  
 6060  
 6080  
 6100  
 6120  
 6140  
 6160  
 6180  
 6200  
 6220  
 6240  
 6260  
 6280  
 6300  
 6320  
 6340  
 6360  
 6380  
 6400  
 6420  
 6440  
 6460  
 6480  
 6500  
 6520  
 6540  
 6560  
 6580  
 6600  
 6620  
 6640  
 6660  
 6680  
 6700  
 6720  
 6740  
 6760  
 6780  
 6800  
 6820  
 6840  
 6860  
 6880  
 6900  
 6920  
 6940  
 6960  
 6980  
 7000  
 7020  
 7040  
 7060  
 7080  
 7100  
 7120  
 7140  
 7160  
 7180  
 7200  
 7220  
 7240  
 7260  
 7280  
 7300  
 7320  
 7340  
 7360  
 7380  
 7400  
 7420  
 7440  
 7460  
 7480  
 7500  
 7520  
 7540  
 7560  
 7580  
 7600  
 7620  
 7640  
 7660  
 7680  
 7700  
 7720  
 7740  
 7760  
 7780  
 7800  
 7820  
 7840  
 7860  
 7880  
 7900  
 7920  
 7940  
 7960  
 7980  
 8000  
 8020  
 8040  
 8060  
 8080  
 8100  
 8120  
 8140  
 8160  
 8180  
 8200  
 8220  
 8240  
 8260  
 8280  
 8300  
 8320  
 8340  
 8360  
 8380  
 8400  
 8420  
 8440  
 8460  
 8480  
 8500  
 8520  
 8540  
 8560  
 8580  
 8600  
 8620  
 8640  
 8660  
 8680  
 8700  
 8720  
 8740  
 8760  
 8780  
 8800  
 8820  
 8840  
 8860  
 8880  
 8900  
 8920  
 8940  
 8960  
 8980  
 9000  
 9020  
 9040  
 9060  
 9080  
 9100  
 9120  
 9140  
 9160  
 9180  
 9200  
 9220  
 9240  
 9260  
 9280  
 9300  
 9320  
 9340  
 9360  
 9380  
 9400  
 9420  
 9440  
 9460  
 9480  
 9500  
 9520  
 9540  
 9560  
 9580  
 9600  
 9620  
 9640  
 9660  
 9680  
 9700  
 9720  
 9740  
 9760  
 9780  
 9800  
 9820  
 9840  
 9860  
 9880  
 9900  
 9920  
 9940  
 9960  
 9980  
 10000

FIG. 9B

ATTAATTATTAAAAA 1388

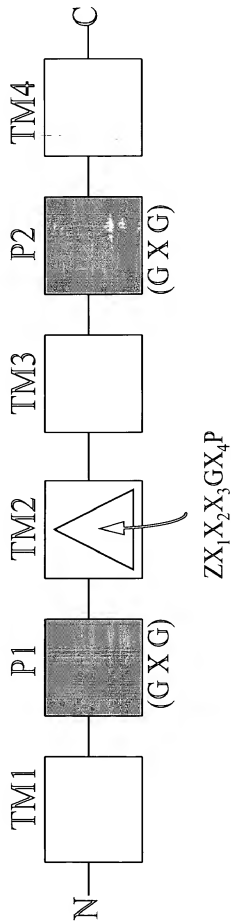


FIG. 10